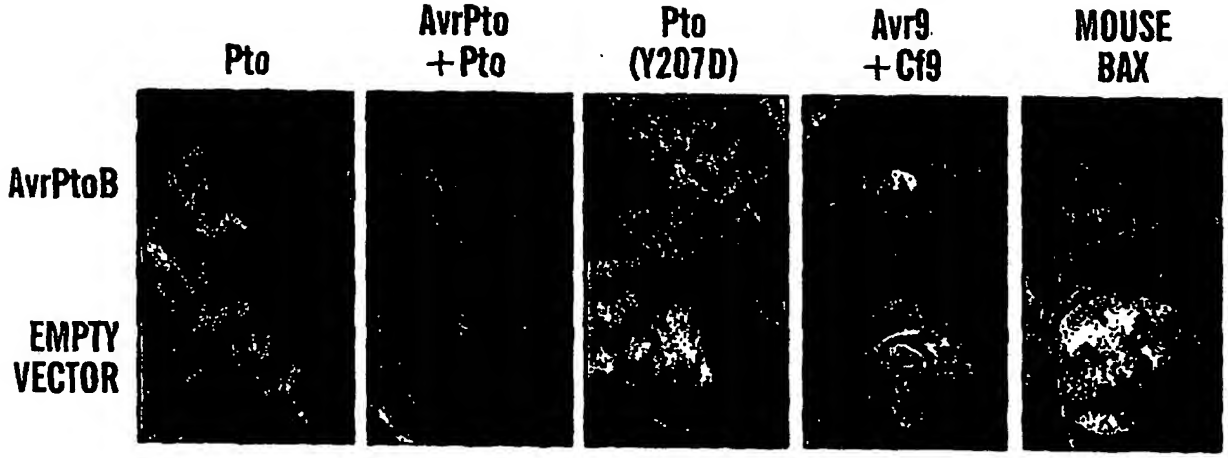


FIG. 1A

FIG. 1B

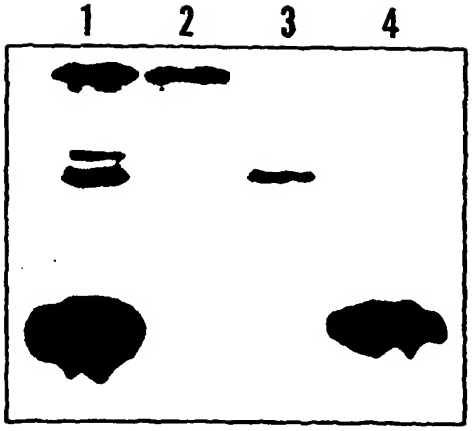


FIG. 1C

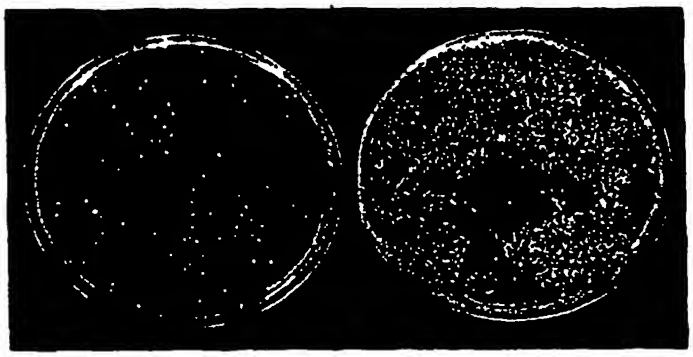

WILD TYPE
AvrPtoB

FIG. 2A

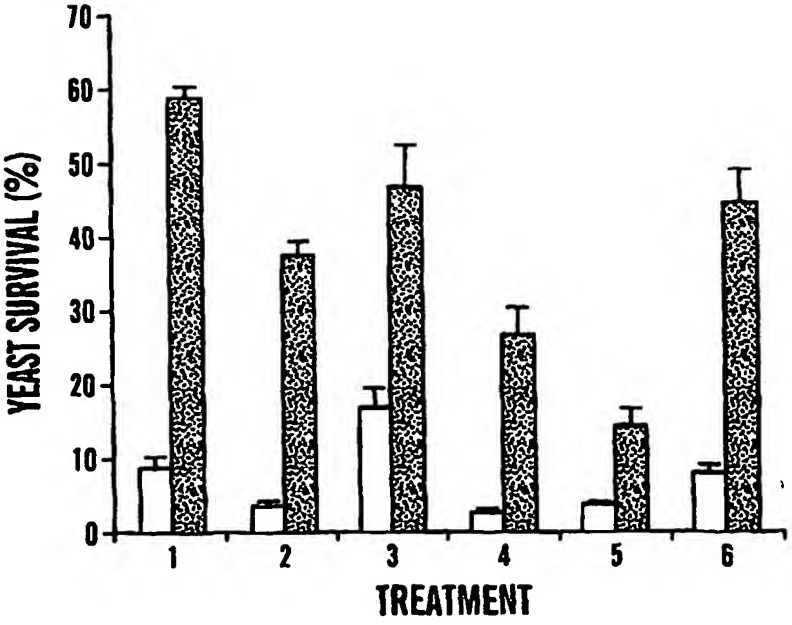

YEAST SURVIVAL (%)
0
10
20
30
40
50
60
70
1
2
3
4
5
6
TREATMENT

FIG. 2B

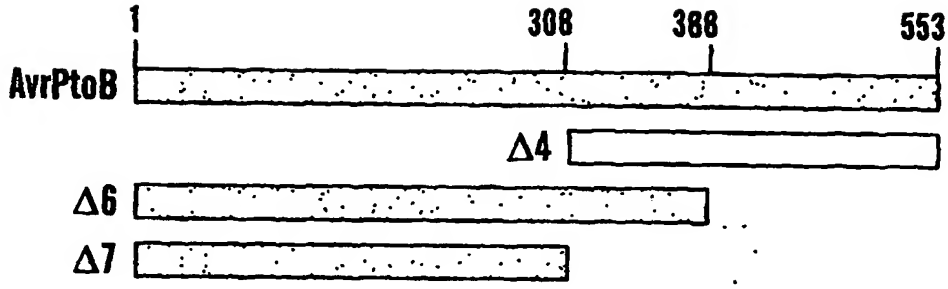


FIG. 3A

	RG-PtoR (Pto/Pto, Prf/Prf)	RG-Prf3 (Pto/Pto, Prf3/Prf3)	RG-Pto11 (pto11/pto11, Prf/Prf)	RG-ptoS (pto/pto, Prf/Prf)
AvrPtoB	+	–	–	–
Δ4	–	–	–	–
Δ6	+	–	+	–*
Δ7	+	–	–	–

FIG. 3B

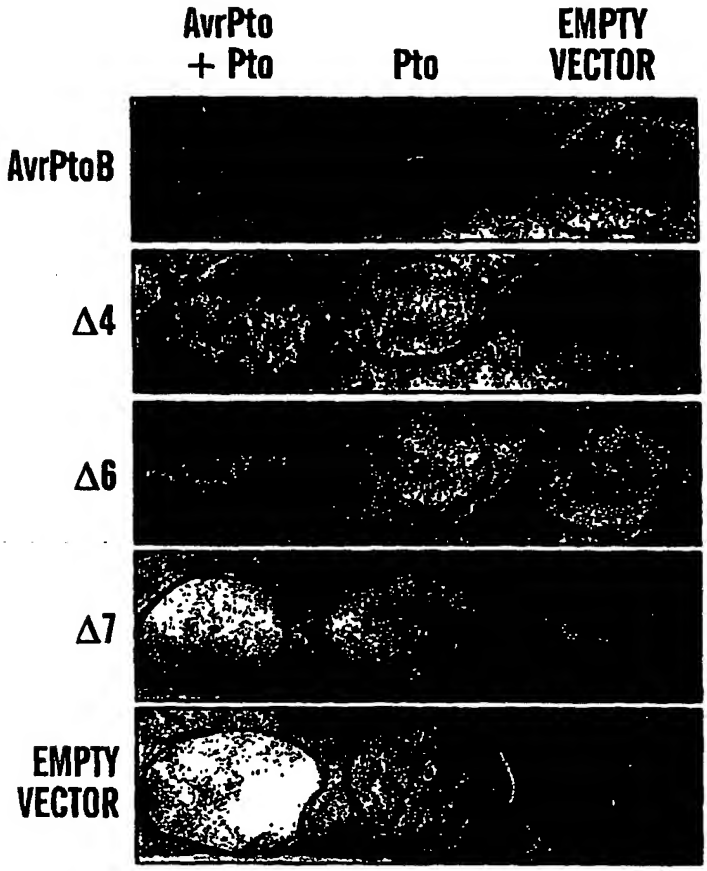


FIG. 4A

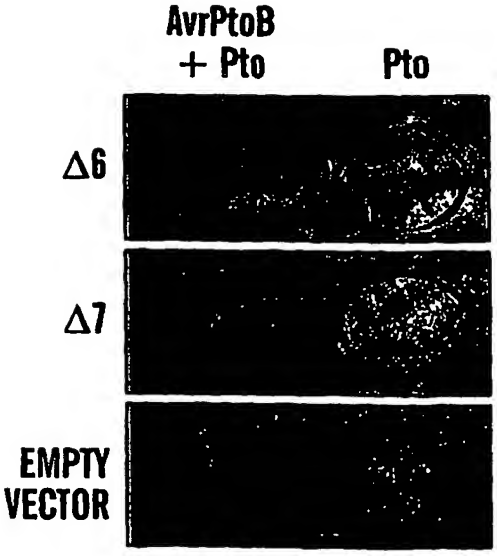


FIG. 4B

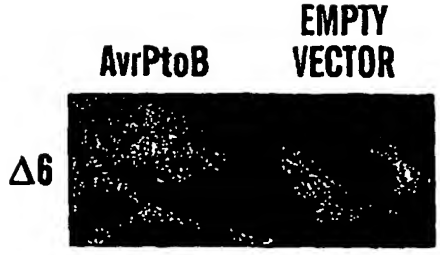


FIG. 4C

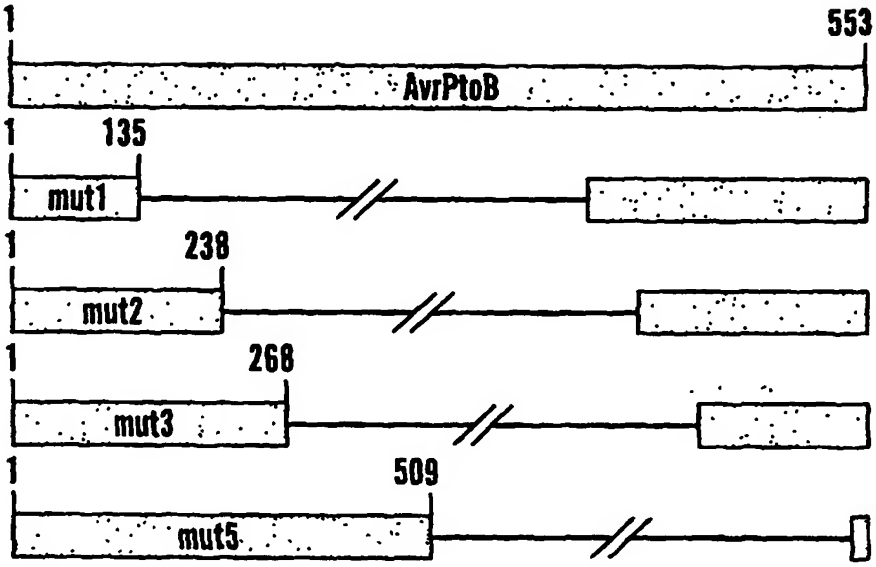


FIG. 5A

	RG-PtoR (*Pto/Pto, Prf/Prf*)	RG-prf3 (*Pto/Pto, prf3/prf3*)	RG-pto11 (*pto11/pto11, Prf/Prf*)	RG-ptoS (*pto/pto, Prf/Prf*)
AvrPtoB	I	D	D	D
mut1	I	D	D	D
mut2	I	D	D	D
mut3	I	D	D	D
mut5	I	D	I	D

FIG. 5B

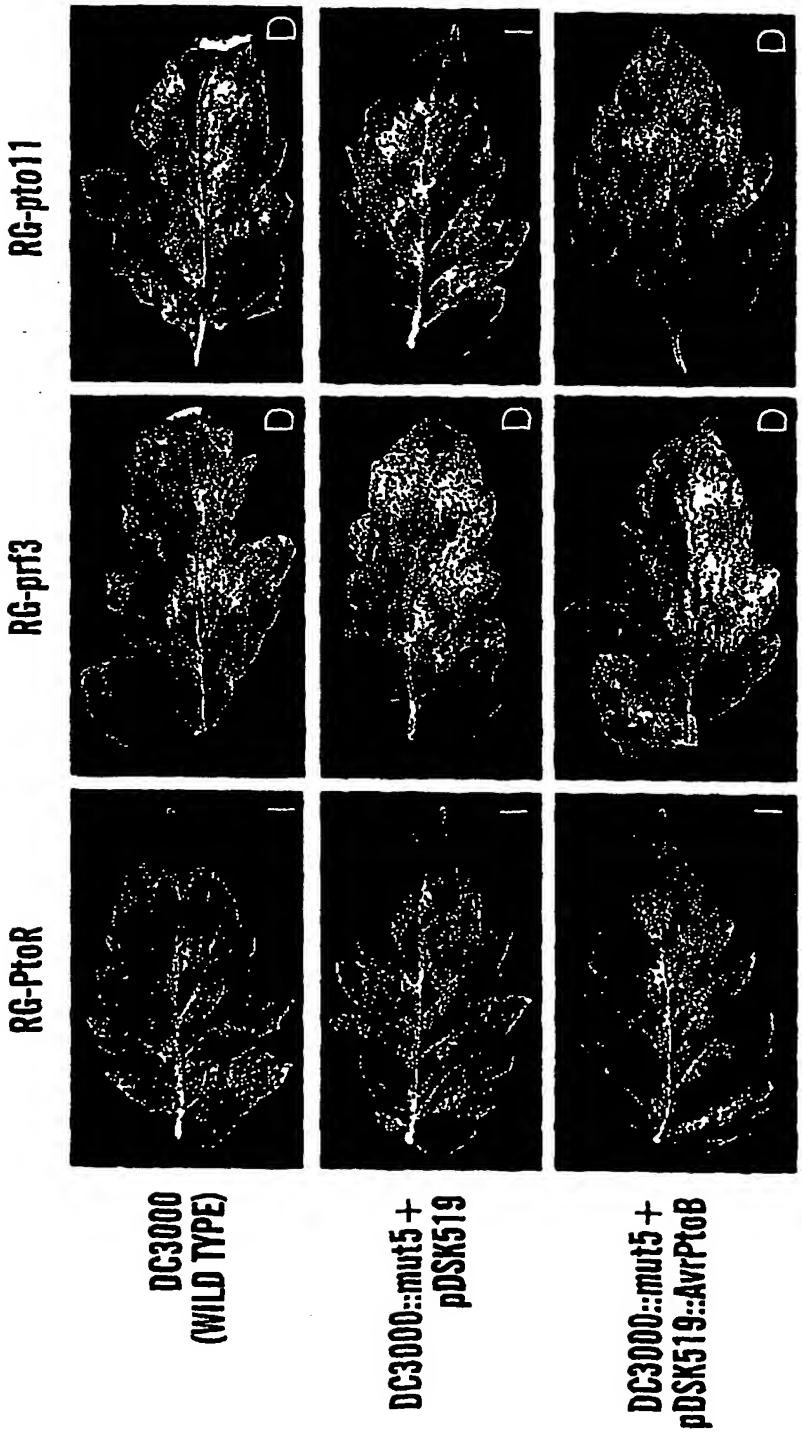

RG-PtoR
RG-prf3
RG-pto11
DC3000 (WILD TYPE)
DC3000::mut5 + pDSK519
DC3000::mut5 + pDSK519::AvrPtoB

FIG. 6A

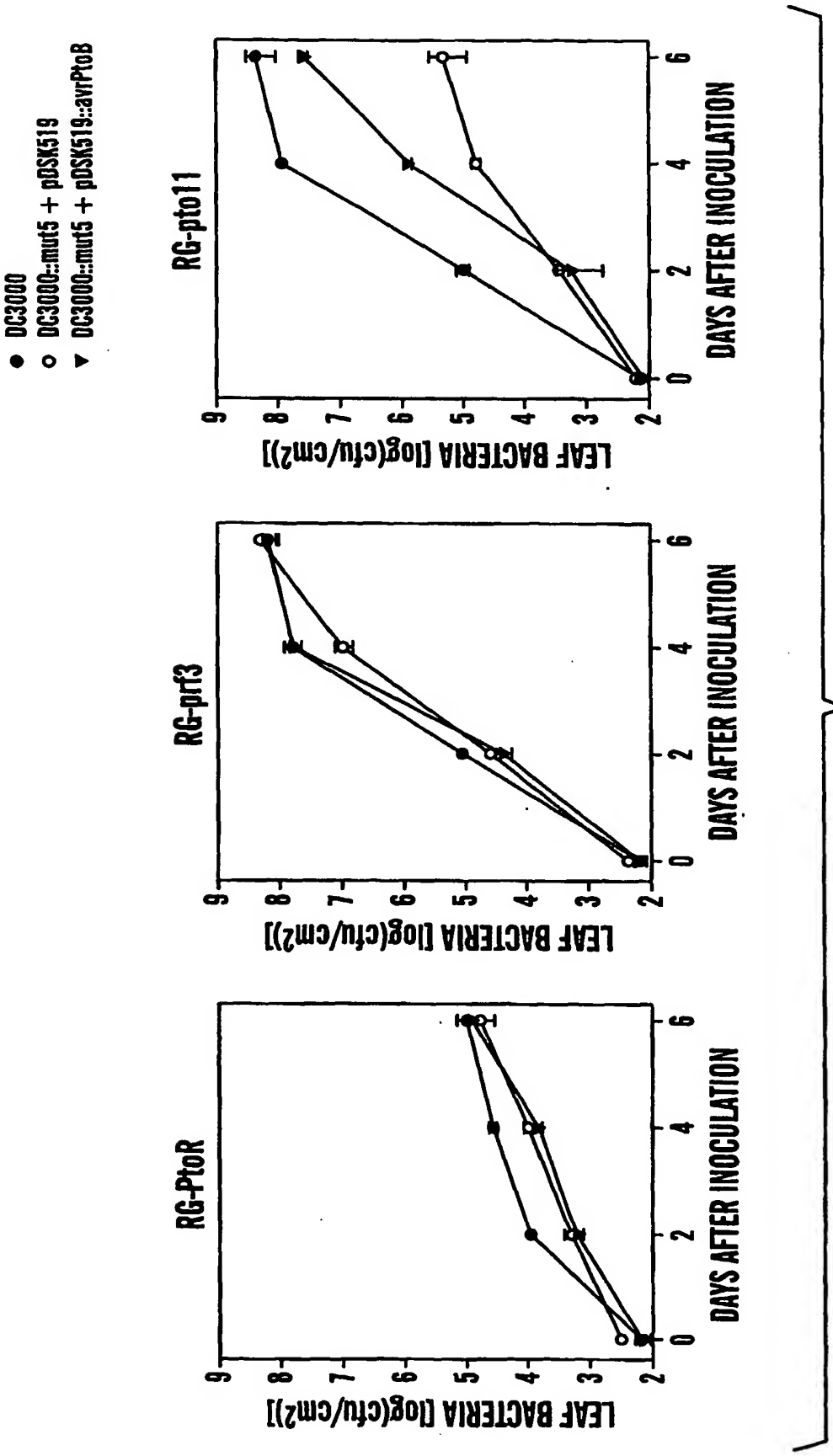

DC3000
DC3000::mut5 + pDSK519
DC3000::mut5 + pDSK519::avrPtoB
RG-pto11
RG-prf3
RG-PtoR
LEAF BACTERIA [log(cfu/cm2)]
DAYS AFTER INOCULATION

FIG. 6B

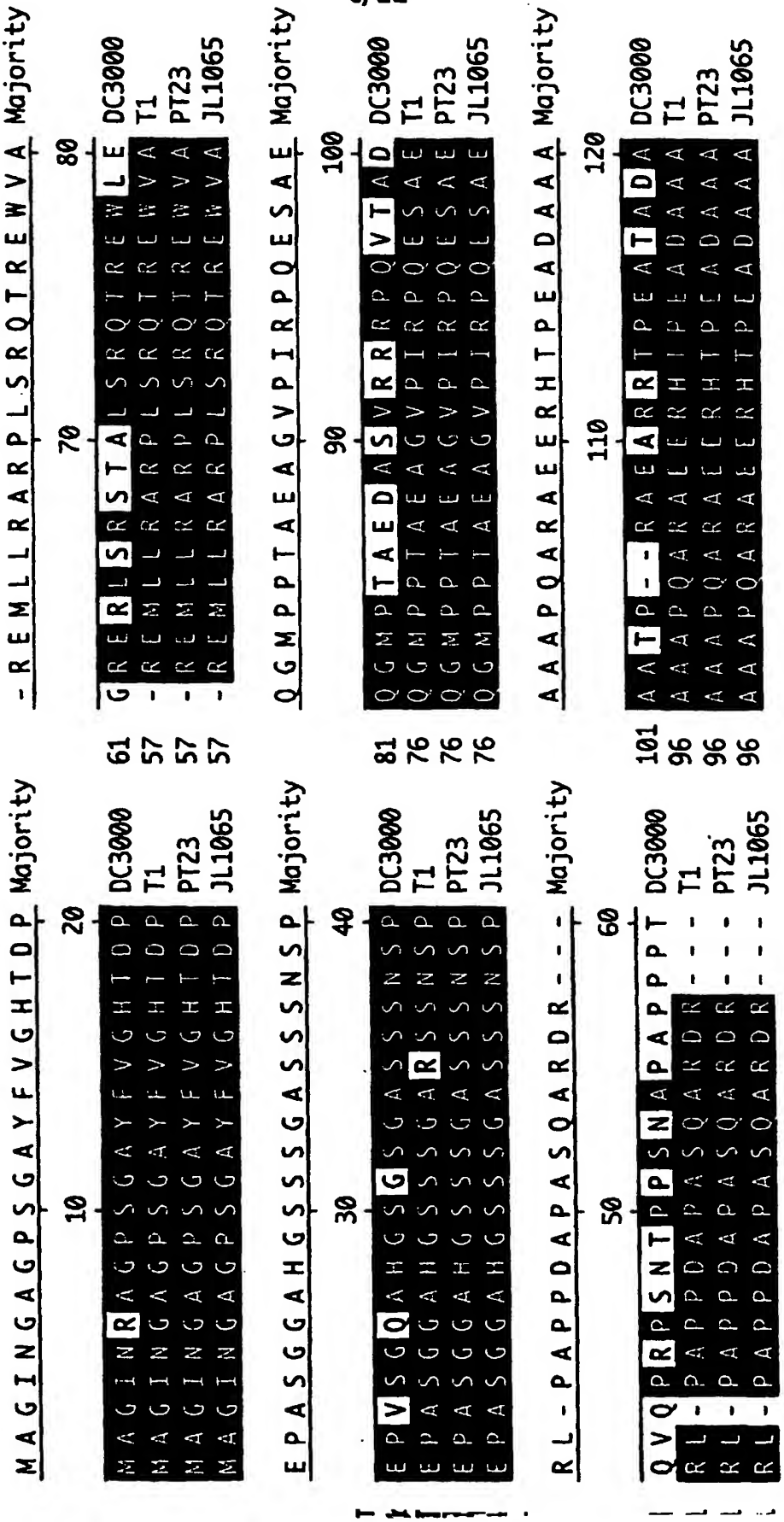


FIG. 7A

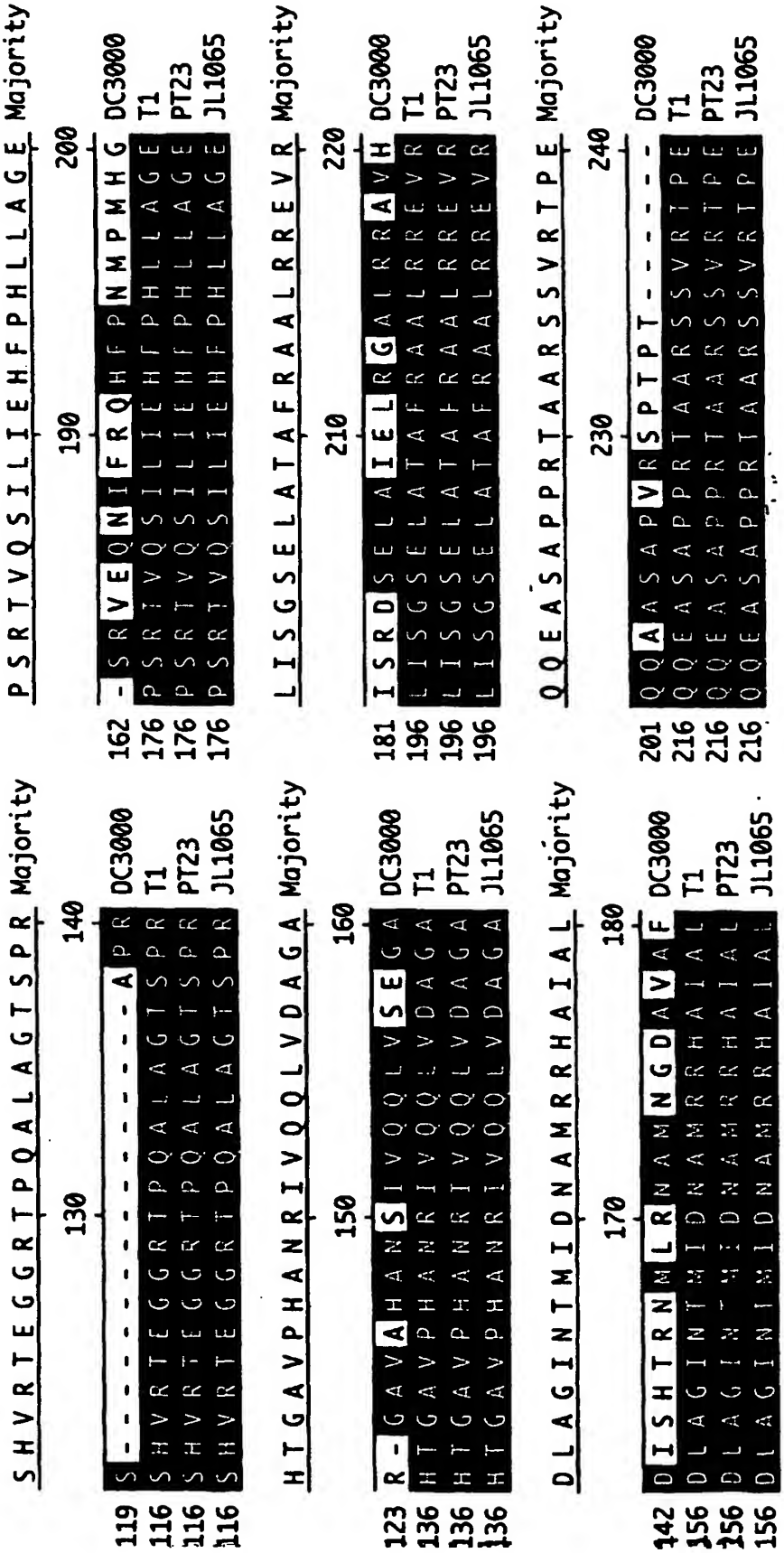

SHVRTEGGRTPQALAGTSPR Majority
130
140
119 S - - - - - - - - - - - - - A P R DC3000
116 SHVRTEGGRTPQALAGTSPR T1
116 SHVRTEGGRTPQALAGTSPR PT23
116 SHVRTEGGRTPQALAGTSPR JL1065
HTGAVPHANRIVQQLVDAGA Majority
150
160
123 R - G A V A H A N S I V Q Q L V S E G A DC3000
136 HTGAVPHANRIVQQLVDAGA T1
136 HTGAVPHANRIVQQLVDAGA PT23
136 HTGAVPHANRIVQQLVDAGA JL1065
DLAGINTMIDNAMRRHAIAL Majority
170
180
142 D I S H T R N M L R N A M N G D A V A F DC3000
156 DLAGINTMIDNAMRRHAIAL T1
156 DLAGIN-MIDNAMRRHAIAL PT23
156 DLAGINIMIDNAMRRHAIAL JL1065
PSRTVQSILIEHFPHLLAGE Majority
190
200
162 - S R V E Q N I F R Q H F P N M P M H G DC3000
176 PSRTVQSILIEHFPHLLAGE T1
176 PSRTVQSILIEHFPHLLAGE PT23
176 PSRTVQSILIEHFPHLLAGE JL1065
LISGSELATAFRAALRREVR Majority
210
220
181 I S R D S E L A I E L R G A I R R A V H DC3000
196 LISGSELATAFRAALRREVR T1
196 LISGSELATAFRAALRREVR PT23
196 LISGSELATAFRAALRREVR JL1065
QQEASAPPRTAARSSVRTPE Majority
230
240
201 Q Q A A S A P V R S P T P T - - - - - - DC3000
216 QQEASAPPRTAARSSVRTPE T1
216 QQEASAPPRTAARSSVRTPE PT23
216 QQEASAPPRTAARSSVRTPE JL1065

FIG. 7B

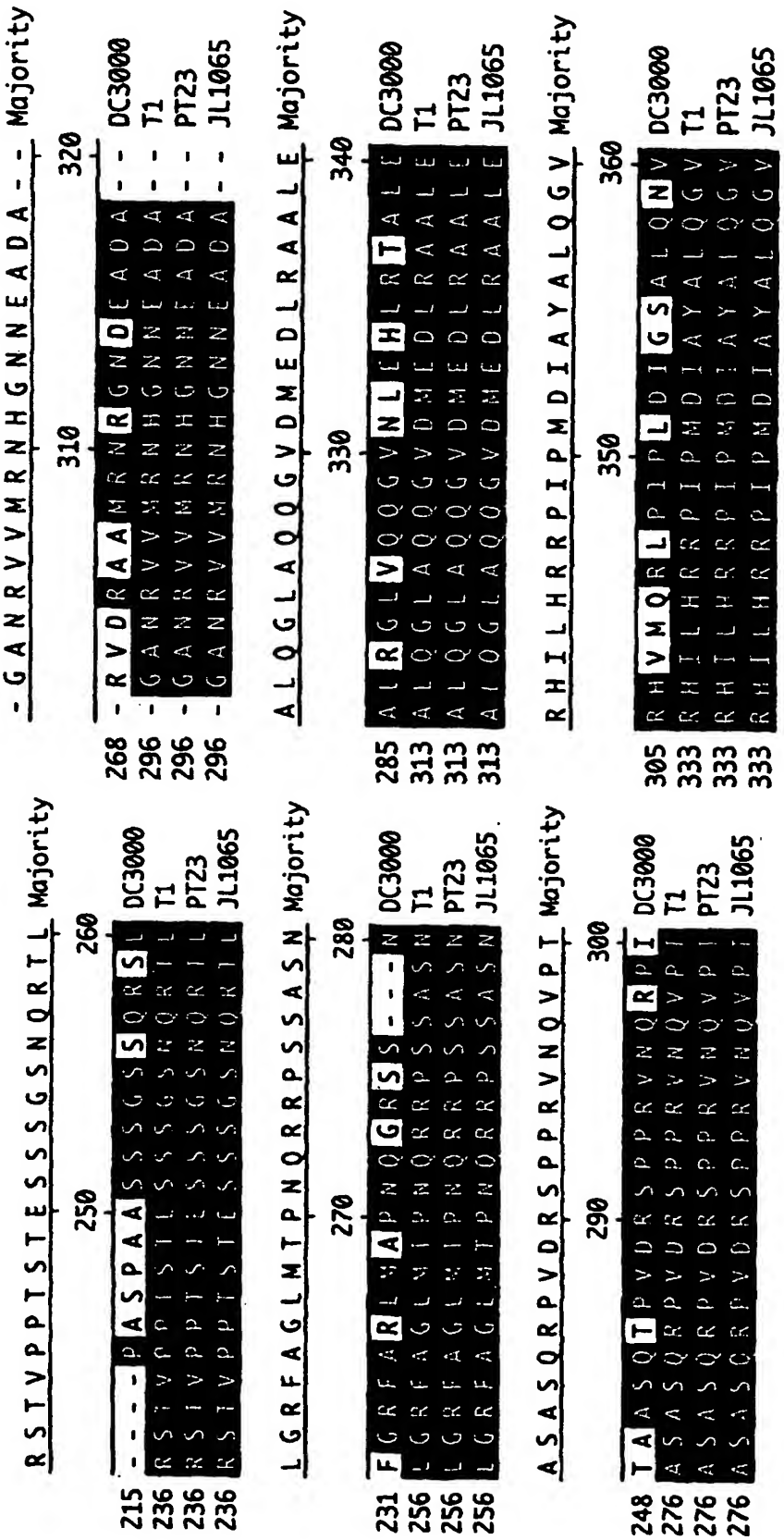

RSTVPPTSTESSSGSNQRTL Majority
250
260
215 ----PASPAASSSSGSSQRSL DC3000
236 RSTVPPTSTLSSSGSNQRIL T1
236 RSIVPPTSTESSSGSNQRIL PT23
236 RSTVPPTSTESSSGSNQRIL JL1065
LGRFAGLMTPNQRRPSSASN Majority
270
280
231 FGRFARLMAPNQGRSS---N DC3000
256 LGRFAGLMIPNQRRPSSASN T1
256 LGRFAGLMIPNQRRPSSASN PT23
256 LGRFAGLMTPNQRRPSSASN JL1065
ASASQRPVDRSPPRVNQVPT Majority
290
300
248 TASASQTPVDRSPPRVNQRPI DC3000
276 ASASQRPVDRSPPRVNQVPI T1
276 ASASQRPVDRSPPRVNQVPI PT23
276 ASASQRPVDRSPPRVNQVPI JL1065
-GANRVVMRNHGNNEADA-- Majority
310
320
268 -RVDRAAMRNRGNDEADA-- DC3000
296 -GANRVVMRNHGNNEADA-- T1
296 -GANRVVMRNHGNNEADA-- PT23
296 -GANRVVNRNHGNNEADA-- JL1065
ALQGLAQQGVDMEDLRAALE Majority
330
340
285 ALRGLVQQGVNLEHLRTALE DC3000
313 ALQGLAQQGVDMEDLRAALE T1
313 ALQGLAQQGVDMEDLRAALE PT23
313 AIQGLAQQGVDMEDLRAALE JL1065
RHILHRRPIPMDIAYALQGV Majority
350
360
305 RHVMQRLPIPLDIGSALQNV DC3000
333 RHILHRRPIPMDIAYALQGV T1
333 RHILHRRPIPMDIAYAIQGV PT23
333 RHILHRRPIPMDIAYALQGV JL1065

FIG. 7C

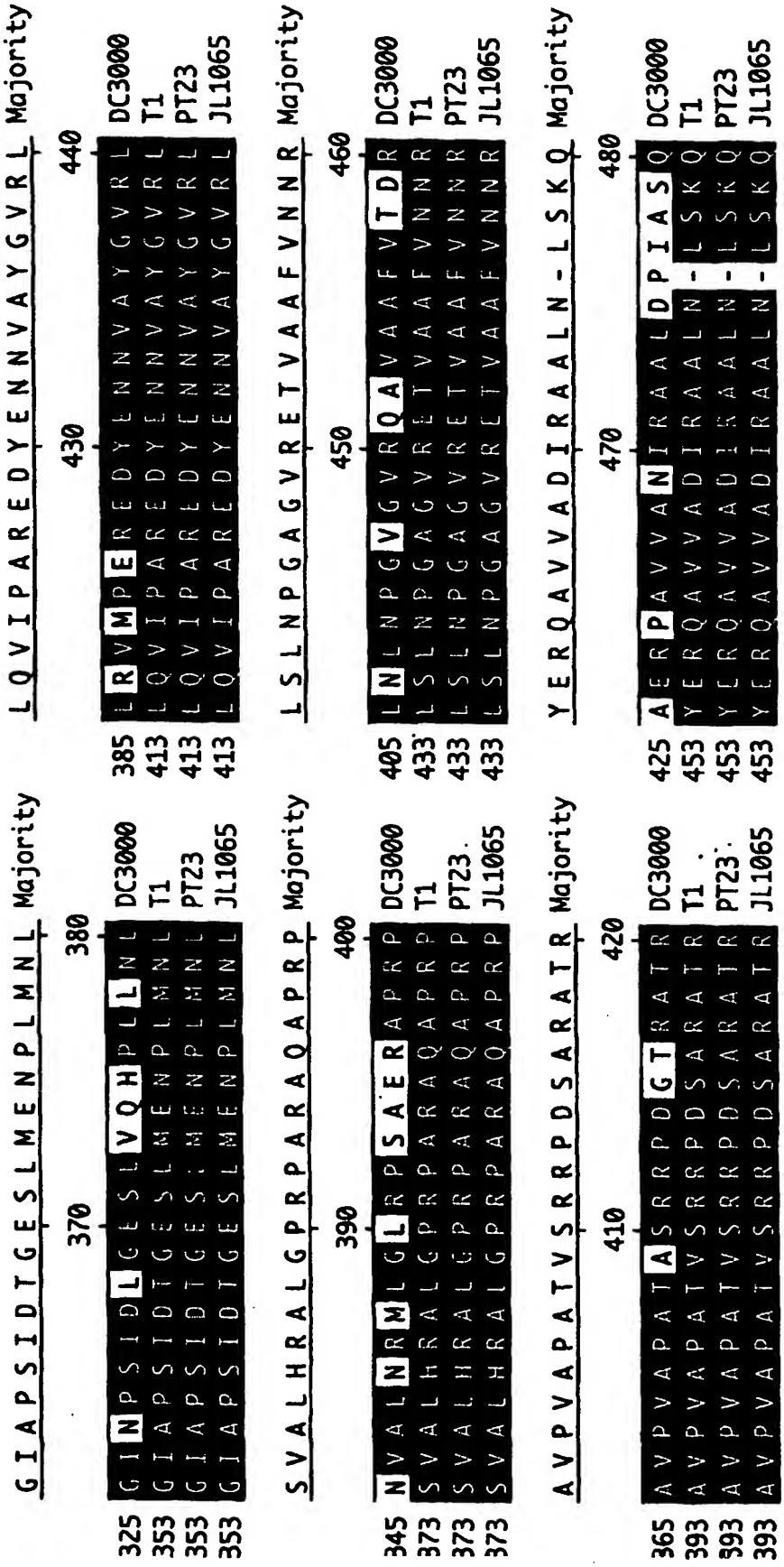

GIAPSIDTGESLMENPLMNL Majority
370
380
325 GINPSIDLGESLVQHPLLNL DC3000
353 GIAPSIDTGESLMENPLMNL T1
353 GIAPSIDTGESLMENPLMNL PT23
353 GIAPSIDTGESLMENPLMNL JL1065
LQVIPAREDYENNVAYGVRL Majority
430
440
385 LRVMPEREDYENNVAYGVRL DC3000
413 LQVIPAREDYENNVAYGVRL T1
413 LQVIPAREDYENNVAYGVRL PT23
413 LQVIPAREDYENNVAYGVRL JL1065
SVALHRALGPRPARAQAPRP Majority
390
400
345 NVALNRMLGLRPSAERAPRP DC3000
373 SVALHRALGPRPARAQAPRP T1
373 SVALHRALGPRPARAQAPRP PT23.
373 SVALHRALGPRPARAQAPRP JL1065
LSLNPGAGVRETVAAFVNNR Majority
450
460
405 LNLNPGVGVRQAVAAFVTDR DC3000
433 LSLNPGAGVRETVAAFVNNR T1
433 LSLNPGAGVRETVAAFVNNR PT23
433 LSLNPGAGVRETVAAFVNNR JL1065
AVPVAPATVSRRPDSARATR Majority
410
420
365 AVPVAPATASRRPDGTRATR DC3000
393 AVPVAPATVSRRPDSARATR T1 .
393 AVPVAPATVSRRPDSARATR PT23.
393 AVPVAPATVSRRPDSARATR JL1065
YERQAVVADIRAALN-LSKQ Majority
470
480
425 AERPAVVANIRAALDPIASQ DC3000
453 YERQAVVADIRAALN-LSKQ T1
453 YERQAVVADIRAALN-LSKQ PT23
453 YERQAVVADIRAALN-LSKQ JL1065

FIG. 7D

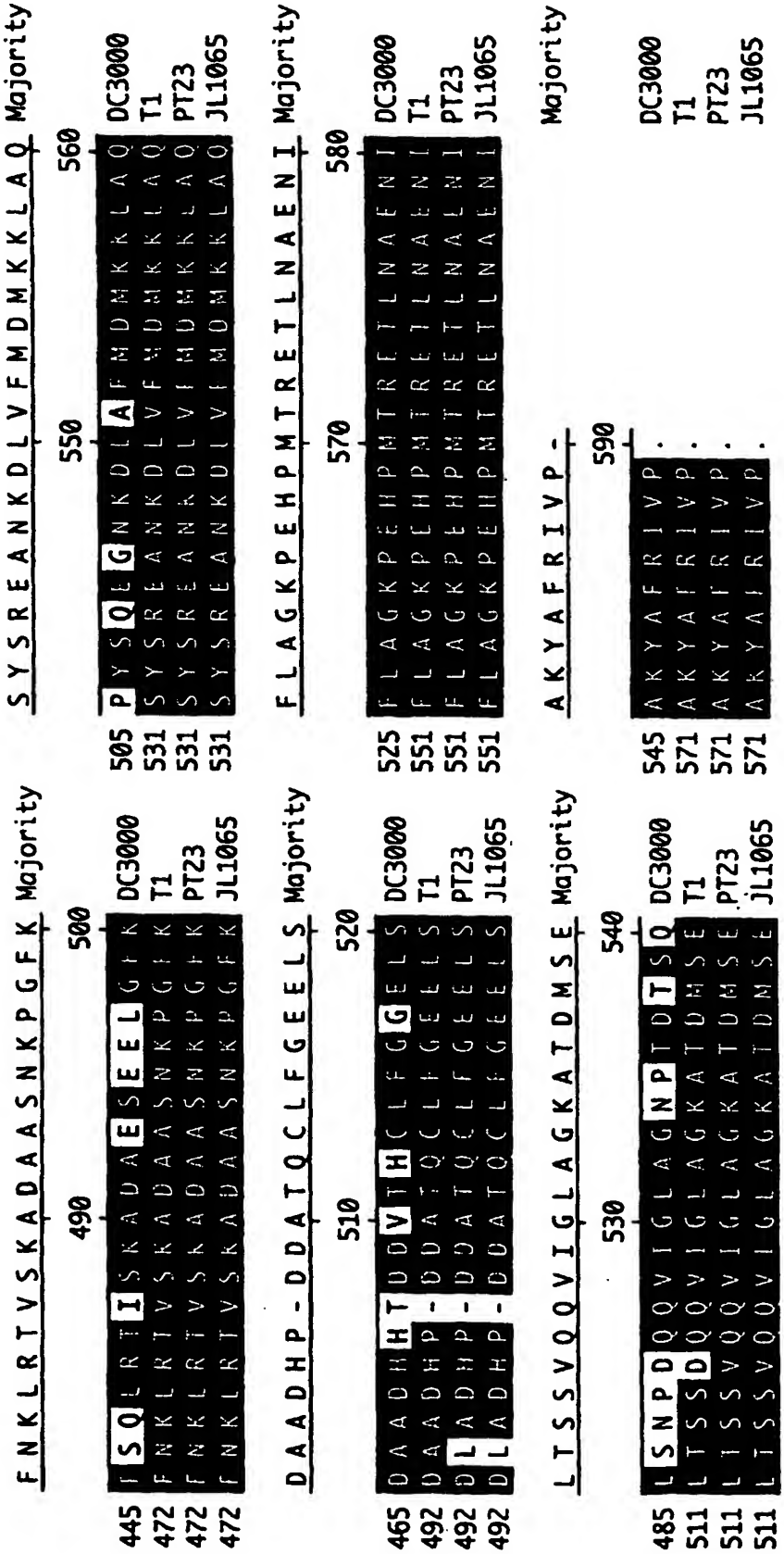

FNKLRTVSKADAASNKPGFK Majority
490
500
445 FNKLRTVSKADAASNKPGFK DC3000
472 FNKLRTVSKADAASNKPGFK T1
472 FNKLRTVSKADAASNKPGFK PT23
472 FNKLRTVSKADAASNKPGFK JL1065
DAADHP-DDATQCLFGEELS Majority
510
520
465 DAADHHTDDVTHCLFGGELS DC3000
492 DAADHP-DDATQCLFGEELS T1
492 DLADHP-DDATQCLFGEELS PT23
492 DLADHP-DDATQCLFGEELS JL1065
LTSSVQQVIGLAGKATDMSE Majority
530
540
485 LSNPDQQVIGLAGNPTDTSQ DC3000
511 LTSSDQQVIGLAGKATDMSE T1
511 LTSSVQQVIGLAGKATDMSE PT23
511 LTSSVQQVIGLAGKATDMSE JL1065
SYSREANKDLVFMDMKKLAQ Majority
550
560
505 PYSQLGNKDLAFMDMKKLAQ DC3000
531 SYSREANKDLVFMDMKKLAQ T1
531 SYSREANKDLVFMDMKKLAQ PT23
531 SYSREANKDLVFMDMKKLAQ JL1065
FLAGKPEHPMTRETLNAENI Majority
570
580
525 FLAGKPEHPMTRETLNAENI DC3000
551 FLAGKPEHPMTRETLNAENI T1
551 FLAGKPEHPMTRETLNALNI PT23
551 FLAGKPEHPMTRETLNAENI JL1065
AKYAFRIVP- Majority
590
545 AKYAFRIVP. DC3000
571 AKYAFRIVP. T1
571 AKYAFRIVP. PT23
571 AKYAFRIVP. JL1065

FIG. 7E

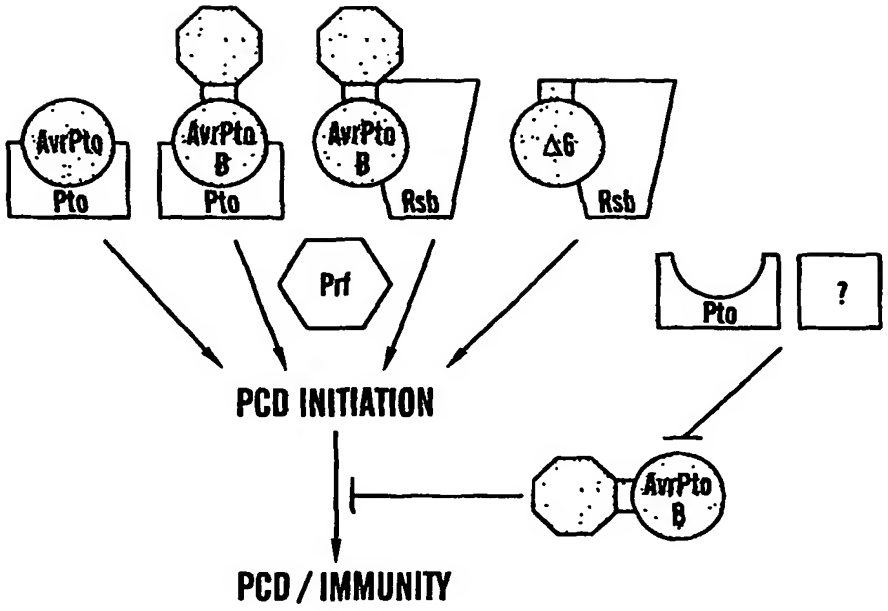

AvrPto
Pto
AvrPto B
Pto
AvrPto B
Rsb
ΔG
Rsb
Prf
Pto
?
PCD INITIATION
AvrPto B
PCD / IMMUNITY

FIG. 8

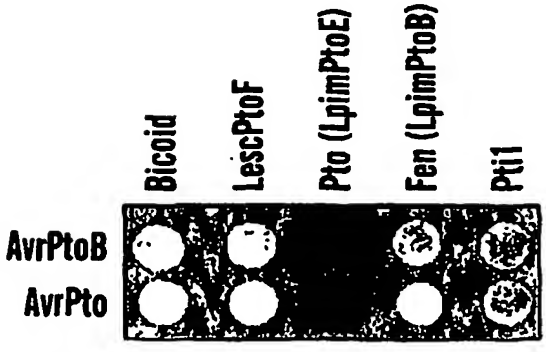

Bicoid
LescPtoF
Pto (LpimPtoE)
Fen (LpimPtoB)
Ptil
AvrPtoB
AvrPto

FIG. 9A

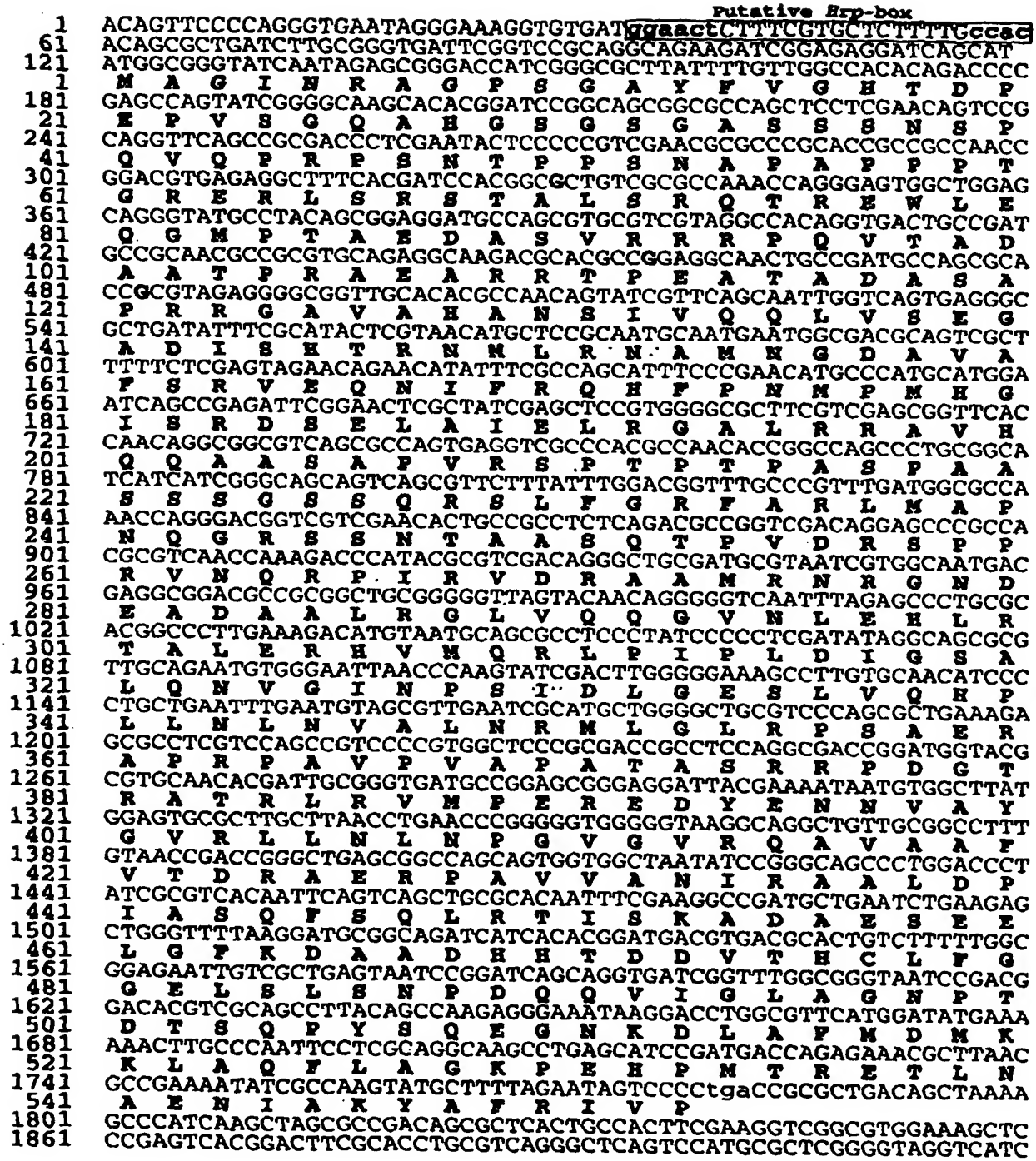


FIG. 9B

- 52% identity of amino acid between AvrPtoB and VirPphA
- Black boxed letters: Putative hrp-box

- Red boxed letters: Computer suggested N-myristoylation site

1.	3- 8	GINRAG
2.	25- 30	GQAHGS
3.	29- 34	GSGSGA
4.	31- 36	GSGASS
5.	33- 38	GASSSN
6.	82- 87	GMPTAE
7.	140-145	GADISH
8.	278-283	GNDEAD
9.	288-293	GVSTTG
10.	294-299	GQFRAL
11.	325-330	GINPSI
12.	353-358	GLRPSA
13.	379-384	GTRATR
14.	412-417	GVRQAV
15.	480-485	GGELSL

- Black bold letters: Amino acid identical with amino acid of VirPphA

- Blue arrow: Fusion point of truncated AvrPtoB with LexA of prey vector
1. 70 AA; *HinP1I*
2. 112 AA; *MspI*
3. 121 AA; *AciI*

FIG. 9B (CONT.)

ALIGNMENT OF THE AMINO ACID SEQUENCES OF AvrPtoB AND VirPpha

BlastX results

Sequences producing significant alignments:	Score (bits)	E Value
gi|5702216|gb|AAD47203.1|AF141883_1 (AF141883) VirPphA [Pse...	500	e-140
gi|5702219|gb|AAD47206.1|AF141883_4 (AF141883) unknown [Pse...	70	6e-11
gi|7512219|pir||T18535 high molecular mass nuclear antigen ...	50	6e-05
gi|15236788|ref|NP_194968.1| (NC_003075) putative protein [...	45	0.002
gi|5420387|emb|CAB46679.1| (AJ243459) proteophosphoglycan [...	45	0.003
gi|6322209|ref|NP_012284.1| (NC_001141) Required for invasi...	44	0.005
gi|14251109|ref|NP_116471.1| (NC_002794) t120 [Tupaia herpe...	43	0.008
gi|4507349|ref|NP_003176.1| (NM_003185) TATA box binding pr...	42	0.013
gi|17546705|ref|NP_520107.1| (NC_003295) PROBABLE TRANSMEMB...	42	0.013
gi|15805485|ref|NP_294181.1| (NC_001263) hypothetical prote...	42	0.013
gi|17487943|ref|XP_036528.2| (XM_036528) serine/arginine re...	42	0.018

>gi|5702216|gb|AAD47203.1|AF141883_1 (AF141883) VirPphA [Pseudomonas syringae pv. phaseolicola] Length = 539

Score = 500 bits (1287), Expect = e-140
Identities = 303/581 (52%), Positives = 368/581 (63%), Gaps = 28/581 (4%)
Frame = +1

```
Query: 1     MAGINRAGPSGAYFVGHTDPEPVSGQAHGSGSGASSSNSPQVQPRPSNTPPSNAPAPPPT 180
              M GIN AGPS  ++.   TD EPV+ + H S    ASS+NSP++ P  S       P  +
Sbjct: 1     MPGINGAGPSNFFWQMRTDGEPVTEREHDSSRSASSANSPELPPPAS---------PAES 51

Query: 181   GRERLSRSTALSRQTREWLEQGMPTAEDASVRRRPQVTADAATPRAEARRTPEATADASA 360
              GR+RL RS+ALSRQTREWLE      A  A V+           ATP AEAR++PEA
Sbjct: 52    GRQRLLRSSALSRQTREWLE-----ATPARVQ--------GATPPAEARQSPEAQ----- 93

Query: 361   PRRGAVAHANSIVQQLVSEGADISHTRNMLRNAANNGDAVAPSRVEQNIFRQHFPNMPMHG 540
                      A  IVQ+LV  GAD+++ R MLRN M+ +AVAPSRVE++I  QHFPNMPM G
Sbjct: 94    -------QAERIVQELVRGGADLNNVRTMLRNVMDNNAVAPSRVERDILLQHFPNMPMTG 146

Query: 541   ISRDSELAIELRGALRRAVHQQAASAPVRSPTPTPASPAASSSGSSQRSLFGRFARLMAP 720
              IS DS LA ELR  LR+ V QQ       R  + TPA  A SSSGSSQRSL GR   LM P
Sbjct: 147   ISSDSVLANELRQRLRQTVRQQ------RIQSSTPARLADSSSGSSQRSLIGRSTMLMTP 200

Query: 721   NQGRSSNTAASQTPVDRSPPRVNQRPIRVDRAAMRNRGNDEADAALRGLVQQGVNLEHLR 900
               +  SS+ AAS+T VDR P  ++     R+  AA  N   ++ + ALR L Q+GV++E LR
Sbjct: 201   GRSSSSSAAASRTSVDRHPQGLDLESARLASAARHNHSANQTNEALRRLTQEGVDMERLR 260

Query: 901   TALERHVNQRLPIPLDIGSALQNVGINPSIDLGESLVQHPLLNLNVALNRMLGLRPSAER 1080
              T+L R++M   P+P D+  AL++VGINP I     SLV HP+LN + ALNRML  R +
Sbjct: 261   TSLGRYIMSLEPLPPDLRRALESVGINPFIPEELSLVDHPVLNFSAALNRMLASRQTTTN 320

Query: 1081  APRPAVPVAPATASRR------------------------PDGT---RATRLRVMPERE 1176
              +P      + A + RR                        P  +   RA RL VMP +
Sbjct: 321   SPELPPLASSAESGRRRLLRSPPLLSGQREWIEQSMRQEAEPQSSRLNRAVRLAVMPPQN 380

Query: 1177  DYENNVAYGVRLLNLNPGVGVRQAVAAFVTDRAERPAVVANIRAALDPIASQPSQLRTIS 1356
              + E+NVAY +RL  LNPG  V + VA+P+TD A R  VV +IRAALD IA QPSQLRTIS
Sbjct: 381   ENEDNVAYAIRLRRLNPGADVSRVVASFITDPAARQQVVNDIRAALD-IAPQPSQLRTIS 439

Query: 1357  KADAESEELGPKDAADHHTDDVTHCLPGGELSLSNPDQQVIGLAGNPTDTSQPYSQEGNK 1536
              KADAESEELGP+DAAD H D+ T CLPG ELSLSNPDQQVIGLA NPTD  QPYSQE NK
Sbjct: 440   KADAESEELGPRDAAD-HPDNATSCLPGEELSLSNPDQQVIGLAVNPTDKPQPYSQEVNK 498

Query: 1537  DLAFMDMKKLAQFLAGKPEHPMTRETLNAENIAKYAFRIVP 1659
               L FMDMKKLAQ+LA KPEHP+ R+ L+A+NIAKYAF+IVP
Sbjct: 499   ALTFMDMKKLAQYLADKPEHPLNRQRLDAKNIAKYAFKIVP 539
```

FIG. 9C

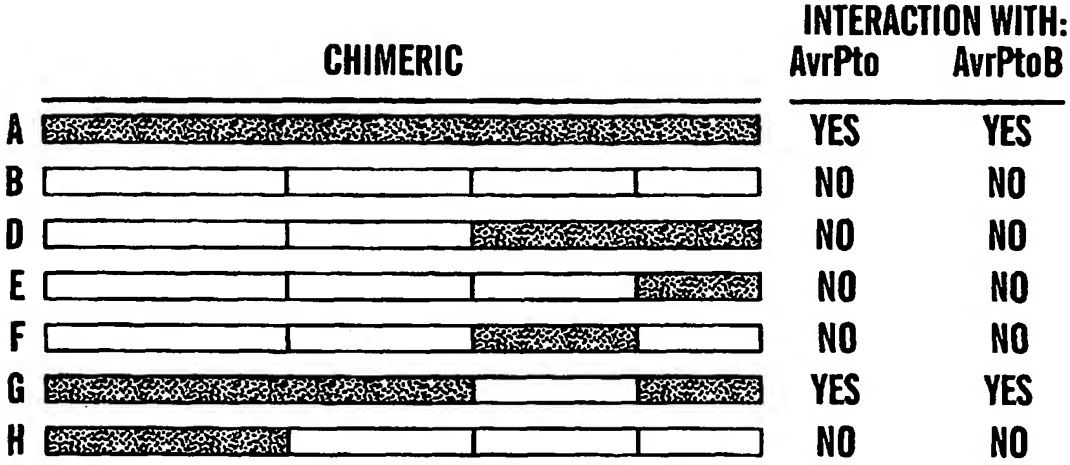


FIG. 10A

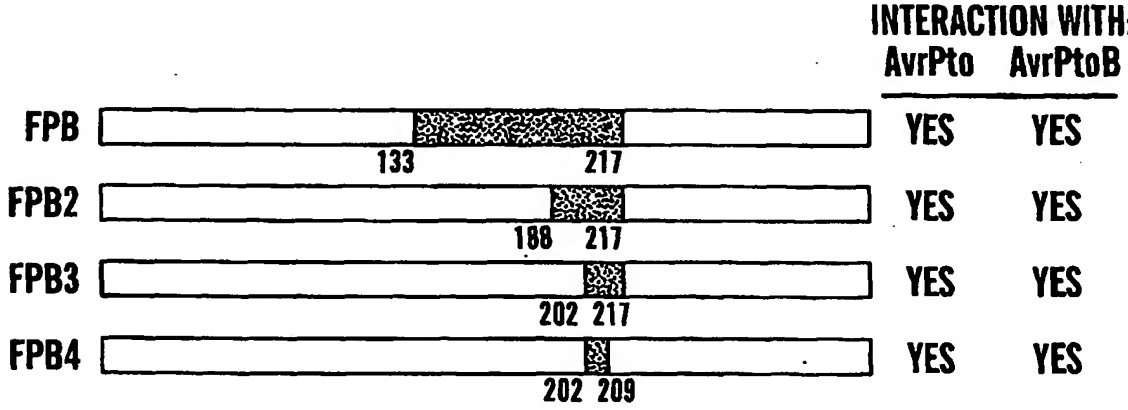


FIG. 10B

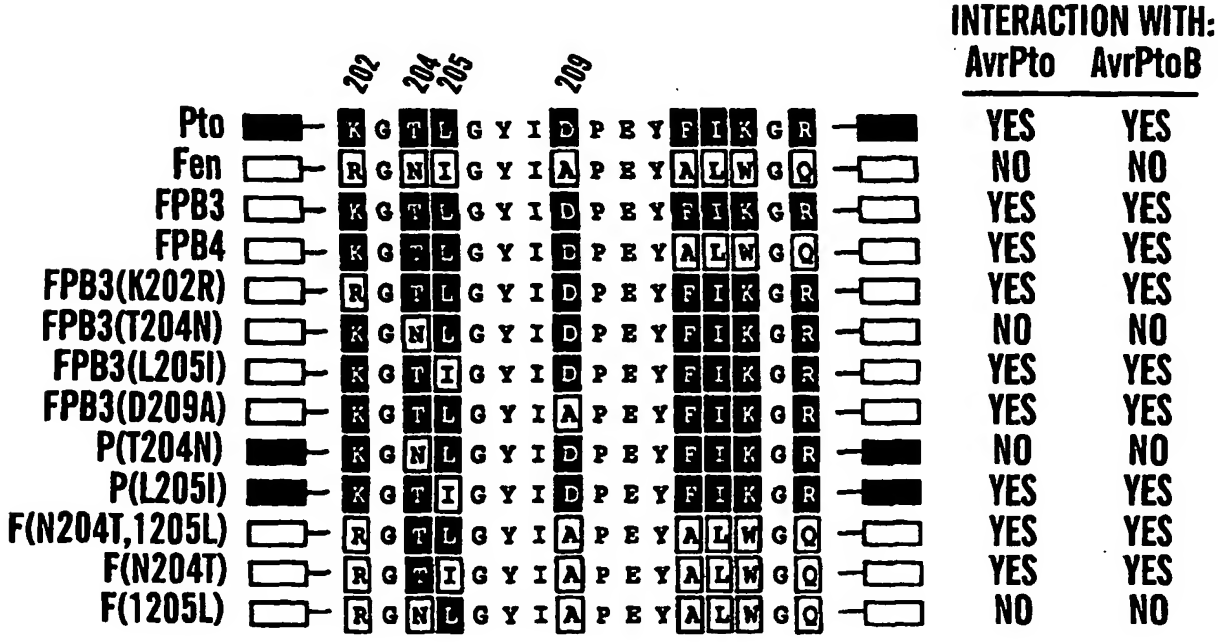


FIG 10C

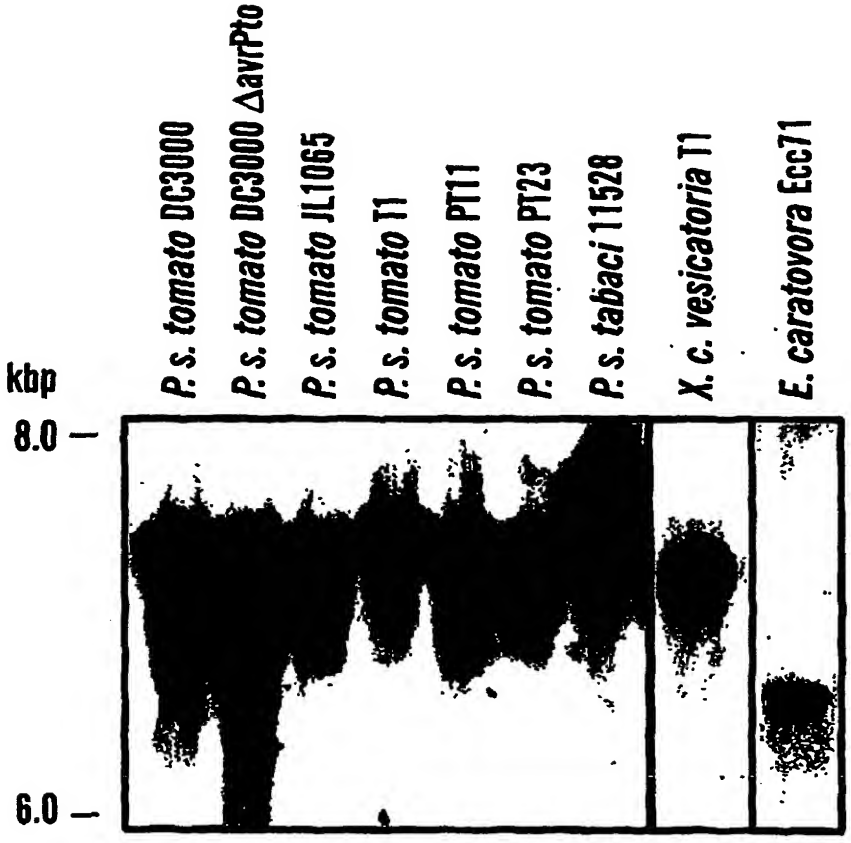


FIG. 11

P. fluorescens (Hrp+, avrPtoB)

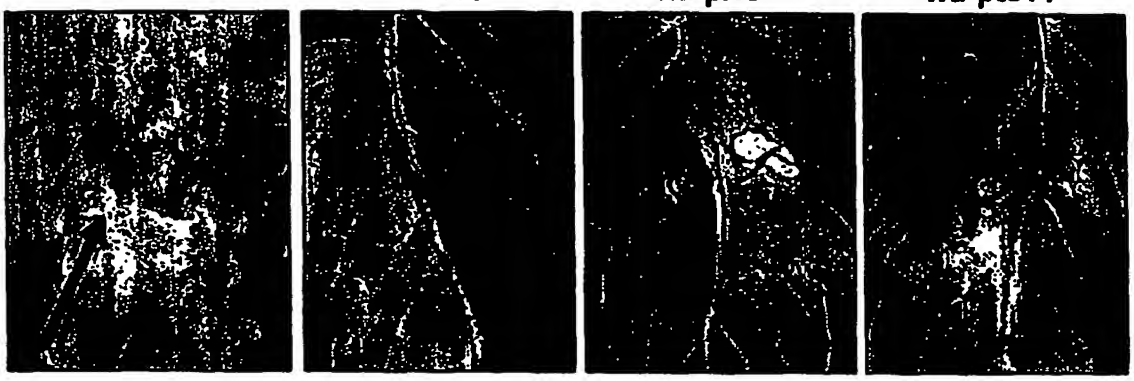


FIG. 12A

Agrobacterium (35S::*avrPtoB*)

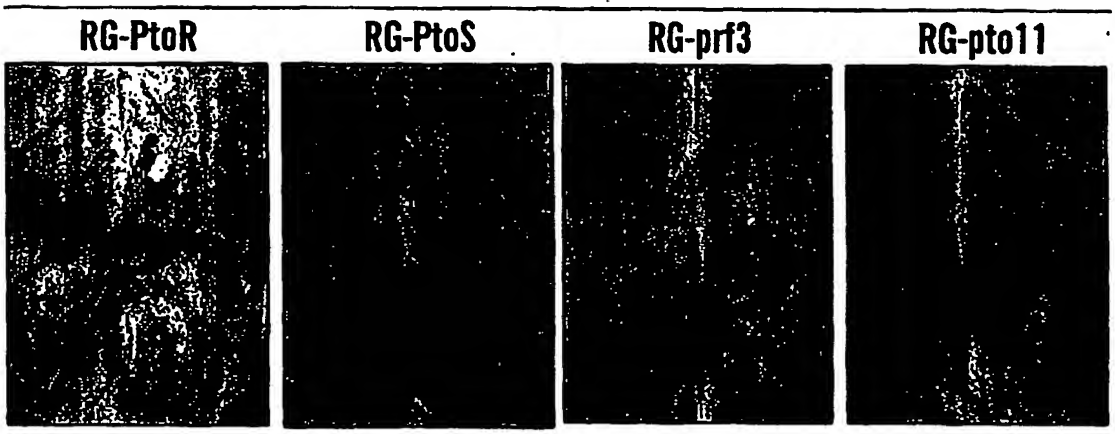
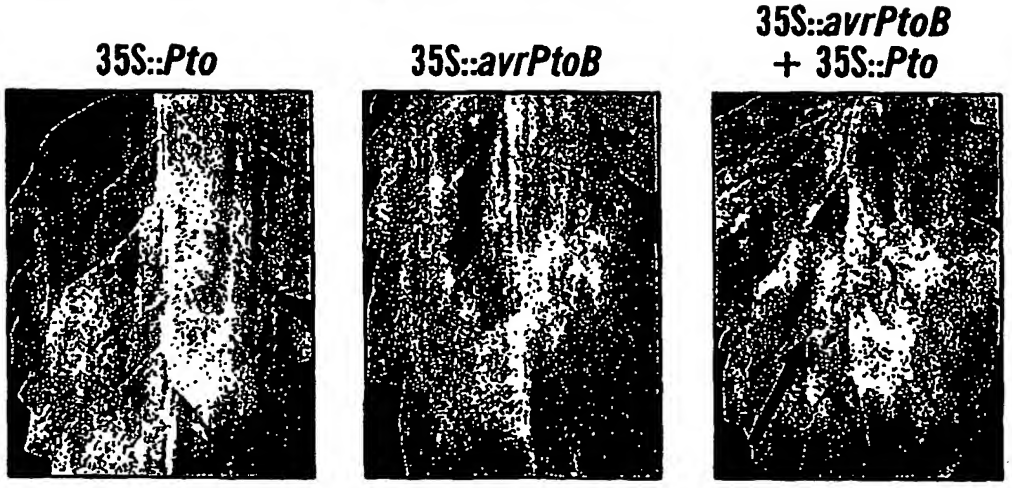


FIG. 12B



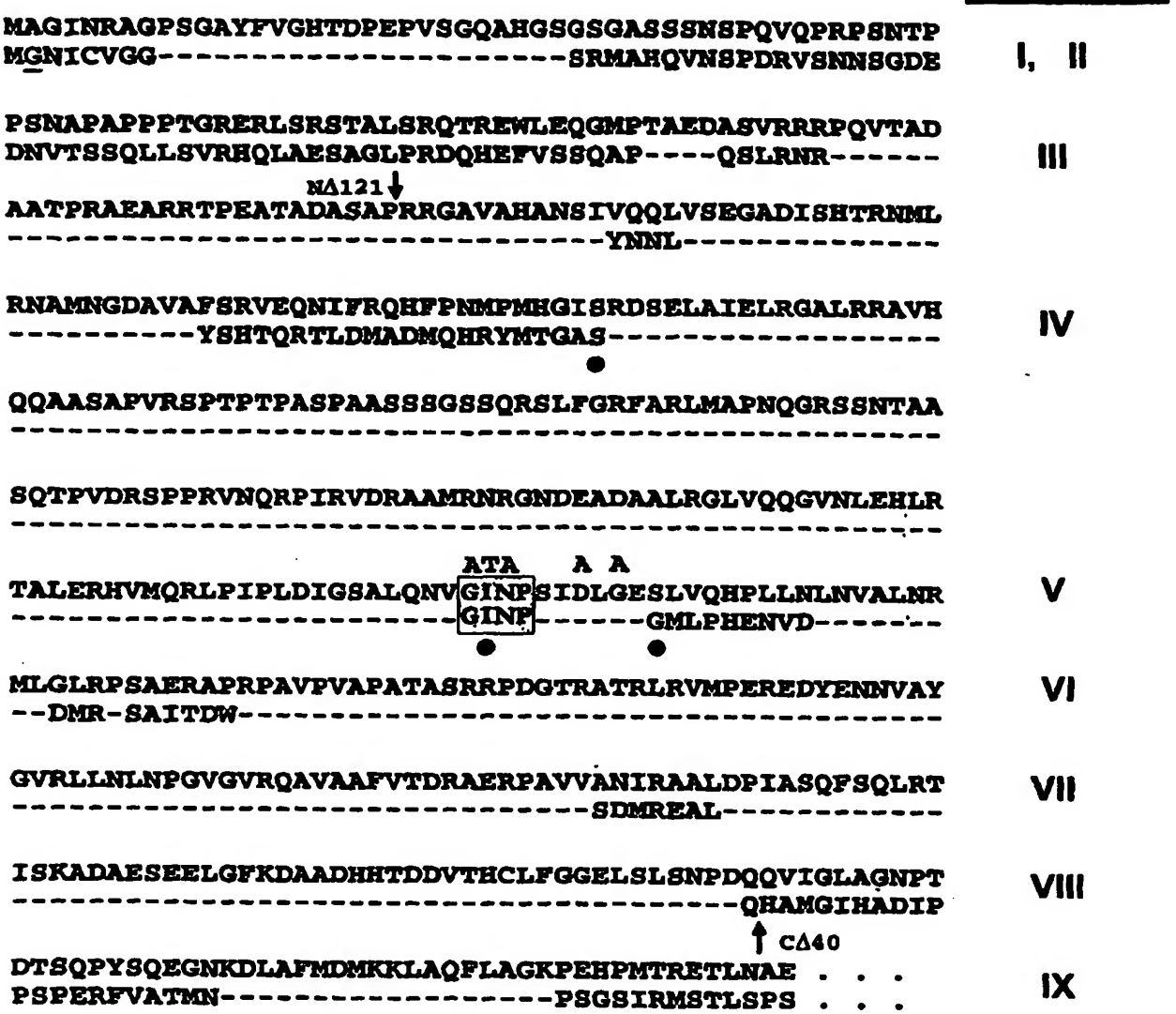


FIG. 13A

Consensus:		SxRxxLxxSxxLxRxxxE	
AvrPto	38	SVRHQLAESAGLPRDQHE	55
AvrPtoB	60	TGRERLSRSTALSRQTRE	77
VirPphA	51	SGRQRLLRSSALSRQTRE	68
AvrRpt2	49	ETRALLATKTVLGRHKIE	66
AvrRps4	38	TTTSIAQASEGLQRPGAT	55
AvrXa10	61	SPAFSAGSFGDLLRQFDP	78
AvrPpiB	41	IEEHVADRLSDLGRPDGG	58
AvrPphF	33	VGQYTLTSIHQLSSEERE	50
AvrBs1	49	RKRVIKENIAALHTSSLE	69
AvrB	33	SQRQLEVYDQCLIGAARW	50
AvrBsT	42	SPSQTSSAFSGLPERPRK	59

FIG. 13B

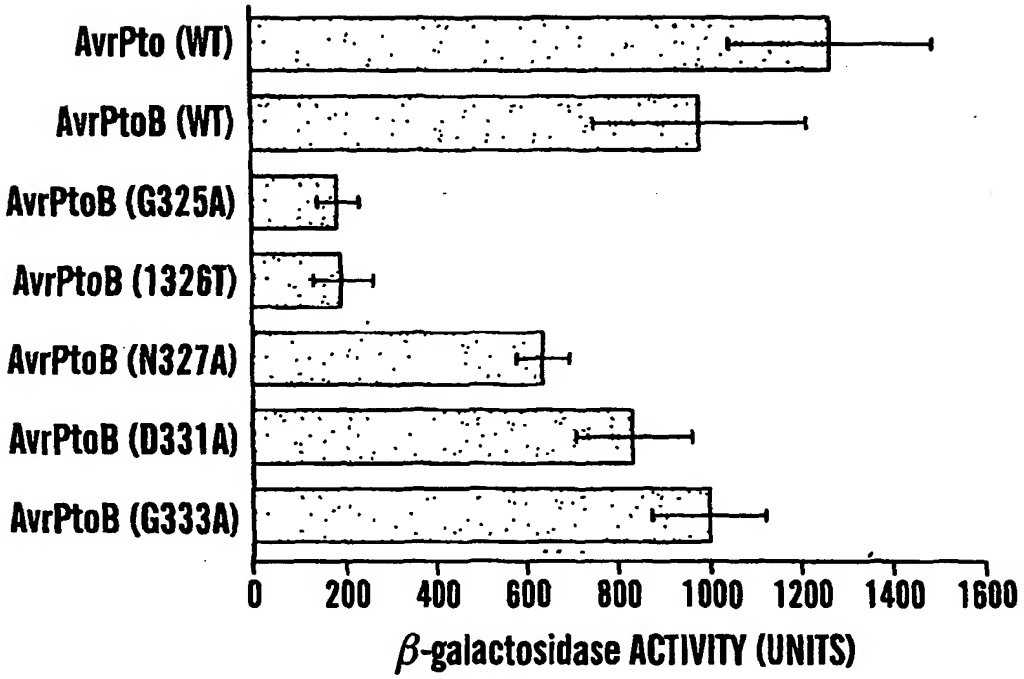

AvrPto (WT)
AvrPtoB (WT)
AvrPtoB (G325A)
AvrPtoB (1326T)
AvrPtoB (N327A)
AvrPtoB (D331A)
AvrPtoB (G333A)
0
200
400
600
800
1000
1200
1400
1600
β-galactosidase ACTIVITY (UNITS)

FIG. 14

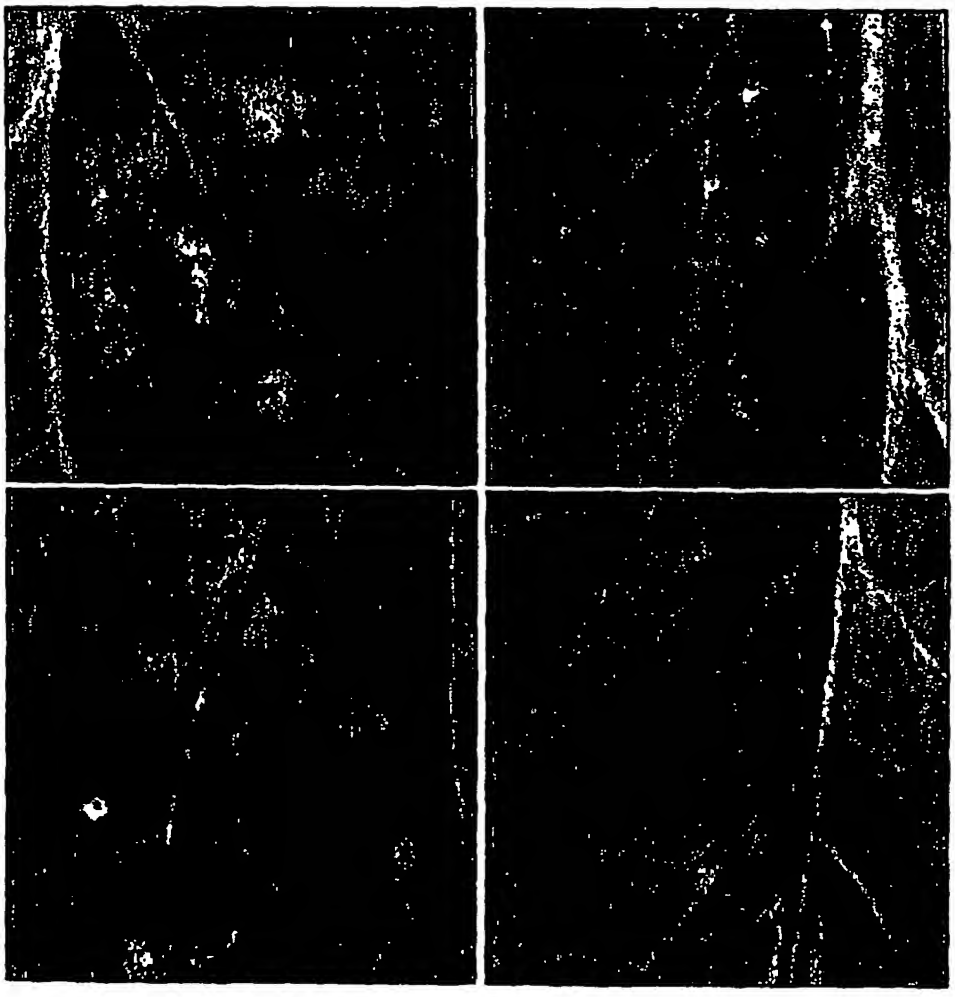

PT11
PT11 (AvrPtoB)
PT11
(AvrPtoB)
1326T MUTANT
PT11
(AvrPtoB)
G33A MUTANT
ALL LEAVES ARE Rio-Grande PtoR(Pto/Pto)

FIG. 15